IN THE CLAIMS:

Applicants, pursuant to revised 37 C.F.R. § 1.121, submit the following amendments to the claims:

1-10 (Cancelled)

11. (Previously added) A method for determining DNA methylation status at a cytosine residue of a CpG sequence, comprising the steps of:

(a) obtaining genomic DNA from a DNA sample to be assayed;

(b) reacting the genomic DNA with sodium bisulfite to convert unmethylated cytosine residues to uracil residues while leaving any 5-methylcytosine residues unchanged to create an exposed bisulfite-converted DNA sample having binding sites for primers specific for the bisulfite-converted DNA sample;

(c) performing a PCR amplification procedure using top strand or bottom strand specific primers;

(d) isolating the PCR amplification products;

(e) performing a primer extension reaction using a Ms-SNuPE primer, labeled dNTPs and *Taq* polymerase, wherein the Ms-SNuPE primer comprises from about a 15 mer to about a 22 mer length primer sequence that is complementary to the bisulfite-converted DNA sample and terminates immediately 5' of the cytosine residue of the CpG sequence to be assayed; and

(f) determining the methylation status at the cytosine residue of the CpG sequence by measuring the incorporation of the labeled dNTPs.

12. (Currently amended) The method of claim 11 wherein the dNTPs are labeled with a label selected from the group consisting of radiolabels, fluorescent labels, ~~phosphorescent labels, enzymic labels, mass labels detectable in a mass spectrometer~~, and combinations thereof.

13. (Currently amended) The method of claim 11 wherein the labeled dNTP for top strand analysis is selected from the group consisting of labeled dCTP, ~~or~~ labeled TTP, and combinations thereof.

14. (Currently amended) The method of claim 11 wherein the labeled dNTP for bottom

strand analysis is selected from the group consisting of labeled dATP, ~~or~~ labeled dGTP, or combinations thereof.

15. (Previously added) The method of claim 11 wherein the isolation step of the PCR products uses an electrophoresis technique.

16. (Previously added) The method of claim 15 wherein the electrophoresis technique uses an agarose gel.

17. (Currently amended) The method of claim 11 wherein the Ms-SNuPE primer sequence comprises a sequence of at least fifteen but no more than twenty five nucleotides of a sequence selected from the group consisting of GaL1 [SEQ ID NO:1], GaL2 [SEQ ID NO:2], GaL4 [SEQ ID NO:3], HuN1 [SEQ ID NO:4], HuN2 [SEQ ID NO:5], HuN3 [SEQ ID NO:6], HuN4 [SEQ ID NO:7], HuN5 [SEQ ID NO:8], HuN6 [SEQ ID NO:9], CaS1 [SEQ ID NO:10], CaS2 [SEQ ID NO:11], CaS4 [SEQ ID NO:12], bisulfite-converted sequences corresponding to SEQ ID NOS:1-12, and complements thereof ~~and the bisulfite-converted equivalents thereof~~.

18. (Currently amended) A Ms-SNuPE primer that terminates immediately 5' upstream of a cytosine residue in a CpG sequence of a CpG island that is frequently hypermethylated in promoter regions of somatic genes in malignant tissue, wherein said Ms-SNuPE primer comprises an oligonucleotide consisting of at least 15 contiguous nucleotides of a gene sequence located immediately 5' upstream from the CpG sequence; and wherein the primer sequence is from about 15 to about 25 nucleotides in length and selected from the group consisting of GaL1 [SEQ ID NO:1], GaL2 [SEQ ID NO:2], GaL4 [SEQ ID NO:3], HuN1 [SEQ ID NO:4], HuN2 [SEQ ID NO:5], HuN3 [SEQ ID NO:6], HuN4 [SEQ ID NO:7], HuN5 [SEQ ID NO:8], HuN6 [SEQ ID NO:9], CaS1 [SEQ ID NO:10], CaS2 [SEQ ID NO:11], CaS4 [SEQ ID NO:12], bisulfite-converted sequences corresponding to SEQ ID NOS:1-12, and complements thereof.

19. (Cancelled).

20. (Cancelled).

21. (Cancelled).

22. (Previously added) The method of claim 11, wherein performing a primer extension reaction comprises simultaneous use of a plurality of unique MS-SNuPE primers, and

wherein each primer comprises from about a 15 mer to about a 22 mer length primer sequence that is complementary to the bisulfite-converted DNA sample and terminates immediately 5' of one of a plurality of unique CpG sequences, whereby the relative methylation status of the plurality of unique CpG sequences can be simultaneously determined.